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Frank Portugal, Ph.D.
Application # 09/027,089

PATENT
Attorney Docket: CAB-001

BOX AF

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re application of:

Frank Portugal

Appl. No.: 09/027,089

Filed: February 02, 1998

For: Method for Identifying Species of
Shigella and E. coli Using Operon
Sequence Analysis

Art Unit: 1655

Examiner: J. Souaya

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On January 30, 2001 _____
signed: Frank Portugal

Appeal and Continuation

Box AF
Commissioner for Patents
Washington DC 20231

Sir:

In response to the Final Office Action (Paper No. 12), applicant submits the following supplemental remarks, which place the application in condition for allowance. A Notice of Appeal was filed January 16, 20001.

Supplemental Remarks

A. New Document Sabat, et. al. Proves the New Claims are Unobvious

In the previous Remarks submitted on January 22, 2001, the Applicant referred to the use of polymerase chain reaction (PCR) method of Sabat et. al. as proof that the new claims are

8132104

unobvious. The Amended claims of January 22, 2001 are intended to cover any process, such as hybridization or PCR, for which an oligonucleotide is selected and used to make discriminations between or among species. In both PCR and hybridization, for example, an oligonucleotide is annealed to a complementary nucleic acid strand as dictated by Chargaff's rules on nucleic acid complementation. These rules specify that a G will hydrogen bond with a C, its complement, and that an A will hydrogen bond with its complement, which can be either a T (DNA) or U (RNA).

The optimal temperature for annealing in both PCR and hybridization reactions is dictated by the melting temperature of the duplex (T_m) formed. Once an optimal temperature is determined, in either PCR or hybridization, the oligonucleotide is annealed to its complementary template. Knowledge of an optimal temperature relative to the T_m is also used to complete each process. For PCR, that involves deliberately exceeding the optimal temperature so that the two strands of the newly formed duplex are fully and completely separated. For hybridization, the use of an optimal temperature relative to the T_m assures the complete separation of those duplexes that do not meet the preset complementary match criteria.

B. The Reference Cited by the Examiner

In the remarks to Examiner filed on January 22, 2001, regarding the citation of Hammond (5,374,718), the Applicant in his previous remarks mentioned (page 6) a comparison of the 16S rRNA sequences for *Chlamydia pneumoniae* (GenBank CHT16SR) and *Chlamydia psittaci* (GenBank E17341). To assist the Examiner is her review of the Reply and Amendment, the Applicant encloses both sets of sequences.
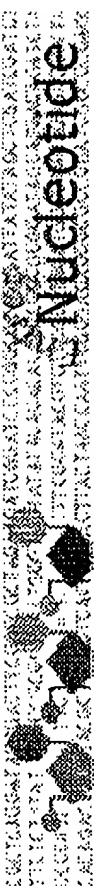
Respectfully submitted,

Date: January 30 , 2001   By: _____

                                           Applicant : Frank Portugal

Encls: GenBank CHT16SR
        Gen Bank E17341

NCBI Sequence Viewer

NCBI

Nucleotide

Search [Nucleotide] for [____] Go Clear

PubMed   Nucleotide   Protein   Genome   Structure   PopSet   Taxonomy   OMIM

Limits   Index   History   Clipboard

[Display] [Default View] as [HTML] [Save] Add to Clipboard

☐ Hide Brief and LinkBar

☐ 1: GI "174111" [GenBank]   Chlamydia pneumoniae 16S ri...   PubMed, Related Sequences, Taxonomy

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LOCUS       CHT16SR       1554 bp    rRNA              BCT       21-SEP-1993
DEFINITION  Chlamydia pneumoniae 16S ribosomal RNA sequence.
ACCESSION   L06108
VERSION     L06108.1  GI:174111
KEYWORDS    16S ribosomal RNA.
SOURCE      Chlamydia pneumoniae (strain TW183) cDNA to rRNA.
ORGANISM    Chlamydophila pneumoniae
            Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
REFERENCE   1  (bases 1 to 1554)
AUTHORS     Gaydos,C.A., Palmer,L., Quinn,T.C., Falkow,S., Brooks,G.F. and
            Eiden,J.J.
TITLE       Phylogenetic relationship of Chlamydia pneumoniae to Chlamydia
            psittaci and Chlamydia trachomatis as determined by analysis of 16S
            ribosomal DNA sequences
JOURNAL     Int. J. Syst. Bacteriol. 43, 610-612 (1993)
MEDLINE     93349759
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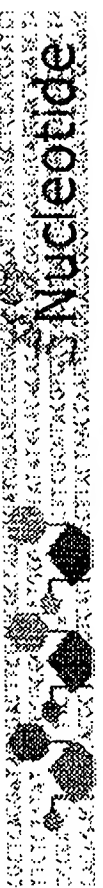
NCBI Sequence Viewer

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  301 gattgagaga ttgaccgcca acactgggac tgagacactg cccagactcc tacgggaggc
  361 tgcagtcgag aatctttcgc aatggacgaa agtctgacga agcgacgccg cgtgtgtgat
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NCBI Sequence Viewer

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PubMed   Nucleotide   Protein   Genome   Structure   PopSet   Taxonomy   OMIM

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Links | Default View   as HTML

Nucleotide

Hide Brief and LinkBar

1: GI "5712024" [GenBank]   Chlamydia psittaci Gp/Ic 16...   Taxonomy, LinkOut

LOCUS   E17341   1548 bp   DNA   PAT   28-JUL-1999
DEFINITION Chlamydia psittaci Gp/Ic 16S rRNA gene.
ACCESSION   E17341
VERSION   E17341.1 GI:5712024
KEYWORDS   JP 1998262679-A/3.
SOURCE   unidentified.
ORGANISM   unidentified
            unclassified.
REFERENCE   1 (bases 1 to 1548)
AUTHORS   Fukushi,H., Hirai,K. and Nakagawa,M.
TITLE   CHLAMYDIA RIBOSOME GENE
JOURNAL   Patent: JP 1998262679-A 3 06-OCT-1998;
            A & T:KK, TOKUYAMA CORP
COMMENT   OS Chlamydia psittaci
            PN JP 1998262679-A/3
            PD 06-OCT-1998
            PF 28-MAR-1997 JP 1997078591
            PI FUKUSHI HIDETO, HIRAI KATSUYA, NAKAGAWA MASANORI PC
            C12N15/09,C07H21/02,C12N1/21,C12Q1/04,C12Q1/68,(C12N15/09, PC
            C12R1:01),
            PC   (C12N1/21,C12R1:19),(C12Q1/68,C12R1:01);
            CC   strandedness: Double;

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